Molecular detection of 16srRNA *methylase* genes among of *Klebsiella pneumoniae* strains isolated from from Qazvin and Tehran provinces, Iran

Background: The increasing pattern of Multi-Drug Resistant (MDR) bacteria have a limited number of therapeutic options especially for nosocomial isolates of *Klebsiella pneumoniae*. One of the important antibiotics that are still used widely for the treatment of serious bacterial infections are Aminoglycosides. Most of Aminoglycoside resistance mechanisms are due to enzyme inactivation by acetyltransferase enzyme and phosphodiesterase nucleotide transferase. Other known mechanisms of resistance to aminoglycosides, include defects in cell permeability, active transport and, rarely, nucleotide substitution in the target molecule.

Objectives: This study aimed to determine the frequency of 16srRNA methylase genes in *Klebsiella pneumoniae* strains isolated from clinical samples by PCR, and evaluate the genetic relations of isolates by enterobacterial repetitive intergenic consensus (ERIC)-PCR.

Materials and Methods: A total of 266 *Klebsiella pneumoniae* isolates were collected from hospitals of Qazvin and Tehran, Iran. The identification of isolates was done by standard laboratory methods. Aminoglycosides susceptibility tests were done by Kirby-Bauer method for screening of aminoglycoside-resistant isolates according to the CLSI guideline. MICs for Gentamicin were determined by agar dilution method. PCR amplification were applied to detect the presence of ١٦srRNA methylase genes (including armA،rmtB،rmtC، rmtD، rmtE ، nmpA and rmtA) by using special primers and positive controls. All positive *AMEs* strain were analyzed for clonality by ERIC-PCR.

Results: 172 (64.6%) out of 266 *K. pneumoniae* isolates, were non-susceptible to aminoglycoside compounds, among those 179 (70.5%) and 82 (32.2%) isolates showed high and low-level of aminoglycoside-resistance against kanamycin and amikacin, respectively. MICs results demonstrated high rate of 88.0% for Gentamicin. Of 172 aminoglycoside non-susceptible isolates, 11(6.3%) isolates were positive for presence of armA, whereas all of strains were negative for other 16srRNA methylase genes. ERIC-PCR analizing, demonstrated that 50% of positive strains showed Different DNA banding patterns as independent genotype which followed by three distinct clones including A (26.2%), B (14%), and C (9.9%). These findings confirmed that most of the isolates were not clonally related.

Conclusions: Lower prevalence of antibiotic resistance genes in this study than some similar studies could be due to the type of sample, the sample is examined or community. Thus to control infection and prevent the spread of drug-resistant bacteria requires careful management of medication and detection of resistant isolates is required.

Key words: *Klebsiella pneumonia,* ١٦srRNA methylase genes, Aminoglycosides, Antibiotic resistance